

Serial Number: 09/612,852

ENTERED

CRF Processing Date: 5/19/2001

Edited by: 12

Verified by: 12 (STIC staff)

RECEIVED

#2150 JUN 21 2001

6/21/01
TECH CENTER 1600/290

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as: _____
- ☒ Inserted mandatory headings, specifically: C1507 and C1517
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

1633

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/612,852

DATE: 05/09/2001
 TIME: 11:33:32

Input Set : A:\09612852
 Output Set: N:\CRF3\05092001\I612852.raw

Does Not Comply
 Corrected Diskette Needed

3 <110> APPLICANT: Curiel, David T.
 4 Krasnykh, Victor N.
 6 <120> TITLE OF INVENTION: Modified Adenovirus Containing A Fiber
 7 Replacement Protein
 W--> 8 <130> FILE REFERENCE: D6070CIP
 W--> 9 <140> CURRENT APPLICATION NUMBER: US/09/612,852
 9 <141> CURRENT FILING DATE: 2000-07-10
 10 <150> PRIOR APPLICATION NUMBER: US 09/250,580
 W--> 11 US 60/074,844
 12 <151> PRIOR FILING DATE: 1999-02-16
 W--> 13 1998-02-17
 W--> 14 <160> NUMBER OF SEQ ID: 14
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 40
 18 <212> TYPE: DNA
 19 <213> ORGANISM: artificial sequence
 W--> 20 <220> FEATURE:
 21 <221> NAME/KEY: primer_bind
 22 <223> OTHER INFORMATION: Forward primer FF.F used to amplify segment of the T4
 23 fibritin gene encoding amino acids Ser-229 through
 24 the carboxy terminal Ala-487.
 W--> 25 <400> SEQUENCE: 1
 26 gggaacttga cctcacagaa cgtttatagt cgtttaaatg 40
 28 <210> SEQ ID NO: 2
 29 <211> LENGTH: 37
 30 <212> TYPE: DNA
 31 <213> ORGANISM: artificial sequence
 W--> 32 <220> FEATURE:
 33 <221> NAME/KEY: primer_bind
 34 <223> OTHER INFORMATION: Reverse primer FF.R used to amplify segment of the T4
 35 fibritin gene encoding amino acids Ser-229 through
 36 the carboxy terminal Ala-487.
 W--> 37 <400> SEQUENCE: 2
 38 aggccatggc caatttttgc cggcgataaa aaggtag 37
 40 <210> SEQ ID NO: 3
 41 <211> LENGTH: 53
 42 <212> TYPE: DNA
 43 <213> ORGANISM: artificial sequence
 W--> 44 <220> FEATURE:
 W--> 45 <221> NAME/KEY:
 46 <223> OTHER INFORMATION: synthetic oligo, F5._3Swa.T, for the introduction of
 47 SwaI restriction site
 W--> 48 <400> SEQUENCE: 3
 49 ttggcccat ttaaatgaat cgtttgtgtt atgtttcaac gtgtttattt ttc 53
 51 <210> SEQ ID NO: 4
 52 <211> LENGTH: 61
 53 <212> TYPE: DNA

RAW SEQUENCE LISTING

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54 <213> ORGANISM: artificial sequence
W--> 55 <220> FEATURE:
W--> 56 <221> NAME/KEY:
57 <223> OTHER INFORMATION: synthetic oligo, F5._3Swa.B, for the introduction of
58     SwaI restriction site
W--> 59 <400> SEQUENCE: 4
60 aattgaaaaa taaacacggtt gaaacataac acaaacgatt catttaaattg 50
61 gggccaatat t 61
63 <210> SEQ ID NO: 5
64 <211> LENGTH: 57
65 <212> TYPE: DNA
66 <213> ORGANISM: artificial sequence
W--> 67 <220> FEATURE:
W--> 68 <221> NAME/KEY:
69 <223> OTHER INFORMATION: synthetic oligo, FFBBLL.T
W--> 70 <400> SEQUENCE: 5
71 ggcaggtgga ggcggttcag ggcgaggtgg ctctggcggt ggcggatccg 50
72 gggattt 57
74 <210> SEQ ID NO: 6
75 <211> LENGTH: 57
76 <212> TYPE: DNA
77 <213> ORGANISM: artificial sequence
W--> 78 <220> FEATURE:
W--> 79 <221> NAME/KEY:
80 <223> OTHER INFORMATION: synthetic oligo, FFBBLL.B
W--> 81 <400> SEQUENCE: 6
82 aaatccccgg atccgccacc gccagagcca cctccgcctg aaccgcctcc 50
83 acctgcc 57
85 <210> SEQ ID NO: 7
86 <211> LENGTH: 36
87 <212> TYPE: DNA
88 <213> ORGANISM: artificial sequence
W--> 89 <220> FEATURE:
W--> 90 <221> NAME/KEY:
91 <223> OTHER INFORMATION: synthetic oligo, RGS6H.T
W--> 92 <400> SEQUENCE: 7
93 gatctagagg atcgcatcac catcaccatc actaat 36
95 <210> SEQ ID NO: 8
96 <211> LENGTH: 32
97 <212> TYPE: DNA
98 <213> ORGANISM: artificial sequence
W--> 99 <220> FEATURE:
W--> 100 <221> NAME/KEY:
101 <223> OTHER INFORMATION: synthetic oligo, RGS6H.B
W--> 102 <400> SEQUENCE: 8
103 attagtgatg gtgatggtga tgcgatcctc ta 32
105 <210> SEQ ID NO: 9
106 <211> LENGTH: 27
107 <212> TYPE: DNA

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RAW SEQUENCE LISTING

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161 Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr
162                20                25                30
163 Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
164                35                40                45
165 Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly
166                50                55                60
167 Met Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly
168                65                70                75
169 Asn Leu Thr Ser Gln Asn Val Tyr Ser Arg Leu Asn Glu Ile Asp
170                80                85                90
171 Thr Lys Gln Thr Thr Val Glu Ser Asp Ile Ser Ala Ile Lys Thr
172                95                100               105
173 Ser Ile Gly Tyr Pro Gly Asn Asn Ser Ile Ile Thr Ser Val Asn
174                110               115               120
175 Thr Asn Thr Asp Asn Ile Ala Ser Ile Asn Leu Glu Leu Asn Gln
176                125               130               135
177 Ser Gly Gly Ile Lys Gln Arg Leu Thr Val Ile Glu Thr Ser Ile
178                140               145               150
179 Gly Ser Asp Asp Ile Pro Ser Ser Ile Lys Gly Gln Ile Lys Asp
180                155               160               165
181 Asn Thr Thr Ser Ile Glu Ser Leu Asn Gly Ile Val Gly Glu Asn
182                170               175               180
183 Thr Ser Ser Gly Leu Arg Ala Asn Val Ser Trp Leu Asn Gln Ile
184                185               190               195
185 Val Gly Thr Asp Ser Ser Gly Gly Gln Pro Ser Pro Pro Gly Ser
186                200               205               210
187 Leu Leu Asn Arg Val Ser Thr Ile Glu Thr Ser Val Ser Gly Leu
188                215               220               225
189 Asn Asn Asp Val Gln Asn Leu Gln Val Glu Ile Gly Asn Asn Ser
190                230               235               240
191 Thr Gly Ile Lys Gly Gln Val Val Ala Leu Asn Thr Leu Val Asn
192                245               250               255
193 Gly Thr Asn Pro Asn Gly Ser Thr Val Glu Glu Arg Gly Leu Thr
194                260               265               270
195 Asn Ser Ile Lys Ala Asn Glu Thr Asn Ile Ala Ser Val Thr Gln
196                275               280               285
197 Glu Val Asn Thr Ala Lys Gly Asn Ile Ser Ser Leu Gln Gly Asp
198                290               295               300
199 Val Gln Ala Leu Gln Glu Ala Gly Tyr Ile Pro Glu Ala Pro Arg
200                305               310               315
201 Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu
202                320               325               330
203 Ser Thr Phe Leu Ser Pro Ala Gly Gly Gly Gly Ser Gly Gly Gly
204                335               340               345
205 Gly Ser Gly Gly Gly Gly Ser Arg Gly Ser His His His His His
206                350               355               360
207 His
208 361
210 <210> SEQ ID NO: 14

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RAW SEQUENCE LISTING DATE: 05/09/2001
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Input Set : A:\09612852
Output Set: N:\CRF3\05092001\I612852.raw

211 <211> LENGTH: 9
212 <212> TYPE: PRT
213 <213> ORGANISM: Unknown
W--> 214 <220> FEATURE:
215 <221> NAME/KEY: DOMAIN
216 <223> OTHER INFORMATION: a peptide ligand containing the RGD motif
W--> 217 <400> SEQUENCE: 14
218 Cys Asp Cys Arg Gly Asp Cys Phe Cys
219 5 9

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/612,852

DATE: 05/09/2001

TIME: 11:33:33

Input Set : A:\09612852

Output Set: N:\CRF3\05092001\I612852.raw

L:8 M:283 W: Missing Blank Line separator, <130> field identifier
L:9 M:282 W: Numeric Field Identifier Missing, <140> CURRENT APPLICATION NUMBER: is Added.
L:11 M:259 W: Allowed number of lines exceeded, <150> PRIOR APPLICATION NUMBER:
L:13 M:259 W: Allowed number of lines exceeded, <151> PRIOR FILING DATE:
L:14 M:283 W: Missing Blank Line separator, <160> field identifier
L:20 M:283 W: Missing Blank Line separator, <220> field identifier
L:25 M:283 W: Missing Blank Line separator, <400> field identifier
L:32 M:283 W: Missing Blank Line separator, <220> field identifier
L:37 M:283 W: Missing Blank Line separator, <400> field identifier
L:44 M:283 W: Missing Blank Line separator, <220> field identifier
L:45 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:48 M:283 W: Missing Blank Line separator, <400> field identifier
L:55 M:283 W: Missing Blank Line separator, <220> field identifier
L:56 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:59 M:283 W: Missing Blank Line separator, <400> field identifier
L:67 M:283 W: Missing Blank Line separator, <220> field identifier
L:68 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:70 M:283 W: Missing Blank Line separator, <400> field identifier
L:78 M:283 W: Missing Blank Line separator, <220> field identifier
L:79 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:81 M:283 W: Missing Blank Line separator, <400> field identifier
L:89 M:283 W: Missing Blank Line separator, <220> field identifier
L:90 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:92 M:283 W: Missing Blank Line separator, <400> field identifier
L:99 M:283 W: Missing Blank Line separator, <220> field identifier
L:100 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:102 M:283 W: Missing Blank Line separator, <400> field identifier
L:109 M:283 W: Missing Blank Line separator, <220> field identifier
L:112 M:283 W: Missing Blank Line separator, <400> field identifier
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L:122 M:283 W: Missing Blank Line separator, <400> field identifier
L:129 M:283 W: Missing Blank Line separator, <220> field identifier
L:133 M:283 W: Missing Blank Line separator, <400> field identifier
L:141 M:283 W: Missing Blank Line separator, <220> field identifier
L:145 M:283 W: Missing Blank Line separator, <400> field identifier
L:155 M:283 W: Missing Blank Line separator, <220> field identifier
L:158 M:283 W: Missing Blank Line separator, <400> field identifier
L:214 M:283 W: Missing Blank Line separator, <220> field identifier
L:217 M:283 W: Missing Blank Line separator, <400> field identifier